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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/966,147DATE: 11/07/2001
TIME: 14:24:21Input Set : A:\GENENT.33CPC4Cseqlist.txt
Output Set: N:\CRF3\11072001\I966147.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Presta, Leonard G.
6 Shelton, David L.
7 Urfer, Roman

ENTERED

9 (ii) TITLE OF INVENTION: HUMAN trk RECEPTORS AND NEUROTROPHIC FACTOR INHIBITORS

11 (iii) NUMBER OF SEQUENCES: 41

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: Knobbe, Martens, Olson & Bear, LLP
15 (B) STREET: 620 Newport Center Drive, 16th Floor
16 (C) CITY: Newport Beach
17 (D) STATE: California
18 (E) COUNTRY: USA
19 (F) ZIP: 92660

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
23 (B) COMPUTER: IBM PC compatible
24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25 (D) SOFTWARE: WinPatin (Genentech)

27 (vi) CURRENT APPLICATION DATA:

28 (A) APPLICATION NUMBER: US/09/966,147 *0V*
29 (B) FILING DATE: 27-Sep-2000 *0V*
30 (C) CLASSIFICATION:

C--> 40 (vii) PRIOR APPLICATION DATA:

33 (A) APPLICATION NUMBER: 08/446172
34 (B) FILING DATE: 19-MAY-1995
37 (A) APPLICATION NUMBER: 08/286846
38 (B) FILING DATE: 05-AUG-1994
41 (A) APPLICATION NUMBER: 08/215139
42 (B) FILING DATE: 18-MAR-1994

C--> 44 (viii) ATTORNEY/AGENT INFORMATION:

45 (A) NAME: Dreger, Ginger
46 (B) REGISTRATION NUMBER: 33,055
47 (C) REFERENCE/DOCKET NUMBER: GENENT.33CPC4CC--> 49 (ix) TELECOMMUNICATION INFORMATION: *0V*50 (A) TELEPHONE: (415) 954-4114
51 (B) TELEFAX: (415) 954-4111

53 (2) INFORMATION FOR SEQ ID NO: 1:

55 (i) SEQUENCE CHARACTERISTICS:

56 (A) LENGTH: 3194 base pairs
57 (B) TYPE: Nucleic Acid
58 (C) STRANDEDNESS: Single
59 (D) TOPOLOGY: Linear *0V*W--> 60 (ii) MOLECULE TYPE: nucleic acid *0V*

62 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

65 GGAAGGTTTA AAGAAGAACG CGCAAAGCGC AGGGAAAGGCC TCCCGGCACG 50
67 GGTGGGGGAA AGCGGGCGGT GCAGCGCGGG GACAGGCACT CGGGCTGGCA 100

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69 CTGGCTGCTA GGGATGTCGT CCTGGATAAG GTGGCATGGA CCCGCCATGG 150
 71 CGCGGCTCTG GGGCTCTGC TGGCTGGTTG TGGGCTCTG GAGGGCCGCT 200
 73 TTCGCCTGTC CCACGTCCTG CAAATGCAGT GCCTCTCGGA TCTGGTGCAG 250
 75 CGACCCCTCT CCGGGCATCG TGGCATTTCC GAGATTGGAG CCTAACAGTG 300
 77 TAGATCCTGA GAACATCACC GAAATTTCA TCGCAAACCA GAAAAGGTTA 350
 79 GAAATCATCA ACGAAGATGA TGTTGAAGCT TATGTGGGAC TGAGAAATCT 400
 81 GACAATTGTG GATTCTGGAT TAAAATTTGT GGCTCATAAA GCATTTCTGA 450
 83 AAAACAGCAA CCTGCAGCAC ATCAATTCTA CCCGAAACAA ACTGACGAGT 500
 85 TTGTCTAGGA AACATTTCCG TCACCTTGAC TTGTCTGAAC TGATCCTGGT 550
 87 GGGCAATCCA TTTACATGCT CCTGTGACAT TATGTGGATC AAGACTCTCC 600
 89 AAGAGGCTAA ATCCAGTCCA GACACTCAGG ATTTGTACTG CCTGAATGAA 650
 91 AGCAGCAAGA ATATTCCCT GGCAAACCTG CAGATACCCA ATTGTGGTTT 700
 93 GCCATCTGCA AATCTGGCCG CACCTAACCT CACTGTGGAG GAAGGAAAGT 750
 95 CTATCACATT ATCCCTGTAGT GTGGCAGGTG ATCCGGTTCC TAATATGTAT 800
 97 TGGGATGTTG GTAACCTGGT TTCCAAACAT ATGAATGAAA CAAGCCACAC 850
 99 ACAGGGCTCC TTAAGGATAA CTAACATTTC ATCCGATGAC AGTGGGAAGC 900
 101 AGATCTCTG TGTGGCGGAA AATCTTGATG GAGAAGATCA AGATTCTGTC 950
 103 AACCTCACTG TGCATTTGC ACCAACTATC ACATTTCTCG AATCTCCAAC 1000
 105 CTCAGACCAC CACTGGTGC A TTCCATTCCAC TGTGAAAGGC AACCCAAAAC 1050
 107 CAGCGCTTCA GTGGTTCTAT AACGGGGCAA TATTGAATGA GTCCAATAC 1100
 109 ATCTGTACTA AAATACATGT TACCAATCAC ACGGAGTACC ACGGCTGCCT 1150
 111 CCAGCTGGAT AATCCCACCT ACATGAACAA TGGGGACTAC ACTCTAATAG 1200
 113 CCAAGAATGA GTATGGGAAG GATGAGAAC AGATTCTGC TCACTTCATG 1250
 115 GGCTGGCCCTG GAATTGACGA TGGTGCAAC CCAAATTATC CTGATGTAAT 1300
 117 TTATGAAGAT TATGGAACTG CAGCGAATGA CATCGGGGAC ACCACGAACA 1350
 119 GAAGTAATGA AATCCCTTCC ACAGACGTCA CTGATAAAAC CGGTGGGAA 1400
 121 CATCTCTCGG TCTATGCTGT GGTGGTGATT GCGTCTGTGG TGGGATTTG 1450
 123 CCTTTGGTA ATGCTGTTTC TGCTTAAGTT GGCAAGACAC TCCAAGTTG 1500
 125 GCATGAAAGG CCCAGCCTCC GTTATCAGCA ATGATGATGA CTCTGCCAGC 1550
 127 CCACTCCATC ACATCTCCAA TGGGAGTAAC ACTCCATCTT CTTCGGAAGG 1600
 129 TGGCCCAGAT GCTGTCATTA TTGGAATGAC CAAGATCCCT GTCATTGAAA 1650
 131 ATCCCCAGTA CTTGGCATC ACCAACAGTC AGCTCAAGGCC AGACACATT 1700
 133 GTTCAGCACA TCAAGCGACA TAACATTGTT CTGAAAAGGG AGCTAGGCAG 1750
 135 AGGAGCCTT GGAAAAGTGT TCCTAGCTGA ATGCTATAAC CTCTGTCCCTG 1800
 137 AGCAGGACAA GATCTTGGTG GCAGTGAAGA CCCTGAAGGA TGCCAGTGAC 1850
 139 AATGCACGCA AGGACTTCCA CCGTGAGGCC GAGCTCCTGA CCAACCTCCA 1900
 141 GCATGAGCAC ATCGTCAAGT TCTATGGCGT CTGCGTGGAG GGCGACCCCC 1950
 143 TCATCATGGT CTTTGAGTAC ATGAAGCATG GGGACCTCAA CAAGTCCCTC 2000
 145 AGGGCACACG GCCCTGATGC CGTGCTGATG GCTGAGGGCA ACCCGCCCAC 2050
 147 GGAACGTGACG CAGTCGCAGA TGCTGCATAT AGCCCAGCAG ATCGCCCGG 2100
 149 GCATGGTCTA CCTGGCGTCC CAGCACTTCG TGCAACCGCA TTTGGCCACC 2150
 151 AGGAACGTGCC TGGTCGGGGA GAACTTGTCTG GTGAAAATCG GGGACTTTGG 2200
 153 GATGTCCCGG GACGTGTACA GCACTGACTA CTACAGGGTC GGTGGCCACA 2250
 155 CAATGCTGCC CATTGCGTGG ATGCCTCCAG AGAGCATCAT GTACAGGAAA 2300
 157 TTCACGACGG AAAGCGACGT CTGGAGCCTG GGGGTCGTGT TGTGGGAGAT 2350
 159 TTTCACCTAT GGCAAACAGC CCTGGTACCA GCTGTCAAAC AATGAGGTGA 2400
 161 TAGAGTGTAT CACTCAGGGC CGAGTCCTGC AGCGACCCCCG CACGTGCC 2450
 163 CAGGAGGTGT ATGAGCTGAT GCTGGGGTGC TGGCAGCGAG AGCCCCACAT 2500
 165 GAGGAAGAAC ATCAAGGGCA TCCATACCCCT CCTTCAGAAC TTGGCCAAGG 2550

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167 CATCTCCGGT CTACCTGGAC ATTCTAGGCT AGGGCCCTTT TCCCCAGACC 2600
169 GATCCTTCCC AACGTACTCC TCAGACGGGC TGAGAGGATG AACATCTTT 2650
171 AACTGCCGCT GGAGGCCACC AAGCTGCTCT CCTTCACTCT GACAGTATTA 2700
173 ACATCAAAGA CTCCGAGAAG CTCTCGAGGG AAGCAGTGTG TACTTCTTCA 2750
175 TCCATAGACA CAGTATTGAC TTCTTTTGG CATTATCTCT TTCTCTCTT 2800
177 CCATCTCCCT TGGTTGTTCC TTTTTCTTT TTTAAATTTT CTTTTCTTC 2850
179 TTTTTTTTCG TCTTCCCTGC TTCACGATTTC TTACCCCTTC TTTTGAATCA 2900
181 ATCTGGCTTC TGCATTACTA TTAACTCTGC ATAGACAAAG GCCTTAACAA 2950
183 ACGTAATTG TTATATCAGC AGACACTCCA GTTGCCCCAC CACAACAAAC 3000
185 AATGCCCTGT TGTATTCTCG CCTTTGATGT GGATGAAAAA AAGGGAAAAC 3050
187 AAATATTTC A CTTAAACTTT GTCACCTCTG CTGTACAGAT ATCGAGAGTT 3100
189 TCTATGGATT CACTTCTATT TATTATATT TATTACTGTT CTTATTGTTT 3150
191 TTGGATGGCT TAAGCCTGTG TATAAAAAAA AAAAAAAATC TAGA 3194

193 (2) INFORMATION FOR SEQ ID NO: 2:

195 (i) SEQUENCE CHARACTERISTICS:
196 (A) LENGTH: 822 amino acids
197 (B) TYPE: Amino Acid
198 (D) TOPOLOGY: Linear

200 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

202 Met	Ser	Ser	Trp	Ile	Arg	Trp	His	Gly	Pro	Ala	Met	Ala	Arg	Leu
203 1				5				10					15	
205 Trp	Gly	Phe	Cys	Trp	Leu	Val	Val	Gly	Phe	Trp	Arg	Ala	Ala	Phe
206					20			25					30	
208 Ala	Cys	Pro	Thr	Ser	Cys	Lys	Cys	Ser	Ala	Ser	Arg	Ile	Trp	Cys
209					35			40					45	
211 Ser	Asp	Pro	Ser	Pro	Gly	Ile	Val	Ala	Phe	Pro	Arg	Leu	Glu	Pro
212					50			55					60	
214 Asn	Ser	Val	Asp	Pro	Glu	Asn	Ile	Thr	Glu	Ile	Phe	Ile	Ala	Asn
215					65			70					75	
217 Gln	Lys	Arg	Leu	Glu	Ile	Ile	Asn	Glu	Asp	Asp	Val	Glu	Ala	Tyr
218					80			85					90	
220 Val	Gly	Leu	Arg	Asn	Leu	Thr	Ile	Val	Asp	Ser	Gly	Leu	Lys	Phe
221					95			100					105	
223 Val	Ala	His	Lys	Ala	Phe	Leu	Lys	Asn	Ser	Asn	Leu	Gln	His	Ile
224					110			115					120	
226 Asn	Phe	Thr	Arg	Asn	Lys	Leu	Thr	Ser	Leu	Ser	Arg	Lys	His	Phe
227					125			130					135	
229 Arg	His	Leu	Asp	Leu	Ser	Glu	Leu	Ile	Leu	Val	Gly	Asn	Pro	Phe
230					140			145					150	
232 Thr	Cys	Ser	Cys	Asp	Ile	Met	Trp	Ile	Lys	Thr	Leu	Gln	Glu	Ala
233					155			160					165	
235 Lys	Ser	Ser	Pro	Asp	Thr	Gln	Asp	Leu	Tyr	Cys	Leu	Asn	Glu	Ser
236					170			175					180	
238 Ser	Lys	Asn	Ile	Pro	Leu	Ala	Asn	Leu	Gln	Ile	Pro	Asn	Cys	Gly
239					185			190					195	
241 Leu	Pro	Ser	Ala	Asn	Leu	Ala	Ala	Pro	Asn	Leu	Thr	Val	Glu	Glu
242					200			205					210	
244 Gly	Lys	Ser	Ile	Thr	Leu	Ser	Cys	Ser	Val	Ala	Gly	Asp	Pro	Val
245					215			220					225	

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247 Pro Asn Met Tyr Trp Asp Val Gly Asn Leu Val Ser Lys His Met
248 230 235 240
250 Asn Glu Thr Ser His Thr Gln Gly Ser Leu Arg Ile Thr Asn Ile
251 245 250 255
253 Ser Ser Asp Asp Ser Gly Lys Gln Ile Ser Cys Val Ala Glu Asn
254 260 265 270
256 Leu Val Gly Glu Asp Gln Asp Ser Val Asn Leu Thr Val His Phe
257 275 280 285
259 Ala Pro Thr Ile Thr Phe Leu Glu Ser Pro Thr Ser Asp His His
260 290 295 300
262 Trp Cys Ile Pro Phe Thr Val Lys Gly Asn Pro Lys Pro Ala Leu
263 305 310 315
265 Gln Trp Phe Tyr Asn Gly Ala Ile Leu Asn Glu Ser Lys Tyr Ile
266 320 325 330
268 Cys Thr Lys Ile His Val Thr Asn His Thr Glu Tyr His Gly Cys
269 335 340 345
271 Leu Gln Leu Asp Asn Pro Thr His Met Asn Asn Gly Asp Tyr Thr
272 350 355 360
274 Leu Ile Ala Lys Asn Glu Tyr Gly Lys Asp Glu Lys Gln Ile Ser
275 365 370 375
277 Ala His Phe Met Gly Trp Pro Gly Ile Asp Asp Gly Ala Asn Pro
278 380 385 390
280 Asn Tyr Pro Asp Val Ile Tyr Glu Asp Tyr Gly Thr Ala Ala Asn
281 395 400 405
283 Asp Ile Gly Asp Thr Thr Asn Arg Ser Asn Glu Ile Pro Ser Thr
284 410 415 420
286 Asp Val Thr Asp Lys Thr Gly Arg Glu His Leu Ser Val Tyr Ala
287 425 430 435
289 Val Val Val Ile Ala Ser Val Val Gly Phe Cys Leu Leu Val Met
290 440 445 450
292 Leu Phe Leu Leu Lys Leu Ala Arg His Ser Lys Phe Gly Met Lys
293 455 460 465
295 Gly Pro Ala Ser Val Ile Ser Asn Asp Asp Asp Ser Ala Ser Pro
296 470 475 480
298 Leu His His Ile Ser Asn Gly Ser Asn Thr Pro Ser Ser Ser Glu
299 485 490 495
301 Gly Gly Pro Asp Ala Val Ile Ile Gly Met Thr Lys Ile Pro Val
302 500 505 510
304 Ile Glu Asn Pro Gln Tyr Phe Gly Ile Thr Asn Ser Gln Leu Lys
305 515 520 525
307 Pro Asp Thr Phe Val Gln His Ile Lys Arg His Asn Ile Val Leu
308 530 535 540
310 Lys Arg Glu Leu Gly Glu Gly Ala Phe Gly Lys Val Phe Leu Ala
311 545 550 555
313 Glu Cys Tyr Asn Leu Cys Pro Glu Gln Asp Lys Ile Leu Val Ala
314 560 565 570
316 Val Lys Thr Leu Lys Asp Ala Ser Asp Asn Ala Arg Lys Asp Phe
317 575 580 585
319 His Arg Glu Ala Glu Leu Leu Thr Asn Leu Gln His Glu His Ile

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320	590	595	600
322	Val Lys Phe Tyr Gly Val Cys Val Glu	Gly Asp Pro Leu Ile	Met
323	605	610	615
325	Val Phe Glu Tyr Met Lys His Gly Asp	Leu Asn Lys Phe Leu	Arg
326	620	625	630
328	Ala His Gly Pro Asp Ala Val Leu Met	Ala Glu Gly Asn Pro	Pro
329	635	640	645
331	Thr Glu Leu Thr Gln Ser Gln Met Leu	His Ile Ala Gln Gln	Ile
332	650	655	660
334	Ala Ala Gly Met Val Tyr Leu Ala Ser	Gln His Phe Val His	Arg
335	665	670	675
337	Asp Leu Ala Thr Arg Asn Cys Leu Val	Gly Glu Asn Leu Leu	Val
338	680	685	690
340	Lys Ile Gly Asp Phe Gly Met Ser Arg	Asp Val Tyr Ser Thr	Asp
341	695	700	705
343	Tyr Tyr Arg Val Gly Gly His Thr Met	Leu Pro Ile Arg Trp	Met
344	710	715	720
346	Pro Pro Glu Ser Ile Met Tyr Arg Lys	Phe Thr Thr Glu Ser	Asp
347	725	730	735
349	Val Trp Ser Leu Gly Val Val Leu Trp	Glu Ile Phe Thr Tyr	Gly
350	740	745	750
352	Lys Gln Pro Trp Tyr Gln Leu Ser Asn	Asn Glu Val Ile Glu	Cys
353	755	760	765
355	Ile Thr Gln Gly Arg Val Leu Gln Arg	Pro Arg Thr Cys Pro	Gln
356	770	775	780
358	Glu Val Tyr Glu Leu Met Leu Gly Cys	Trp Gln Arg Glu Pro	His
359	785	790	795
361	Met Arg Lys Asn Ile Lys Gly Ile His	Thr Leu Leu Gln Asn	Leu
362	800	805	810
364	Ala Lys Ala Ser Pro Val Tyr Leu Asp	Ile Leu Gly	
365	815	820	

367 (2) INFORMATION FOR SEQ ID NO: 3:

369 (i) SEQUENCE CHARACTERISTICS:

370 (A) LENGTH: 1870 base pairs
371 (B) TYPE: Nucleic Acid
372 (C) STRANDEDNESS: Single
373 (D) TOPOLOGY: Linear

375 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

378	GGAAGGTTA AAGAAGAAC	CGCAAAGCGC	AGGAAGGCC	TCCCAGGCACG	50
380	GGTGGGGAA AGCGGCCGGT	GCAGCGCGGG	GACAGGCACT	CGGGCTGGCA	100
382	CTGGCTGCTA GGGATGTCGT	CCTGGATAAG	GTGGCATGGA	CCCGCCATGG	150
384	CGCGGCTCTG GGGCTTCTGC	TGGCTGGTTG	TGGCTTCTG	GAGGGCCGCT	200
386	TTCGCCTGTC CCACGTCCTG	CAAATGCAGT	GCCTCTCGGA	TCTGGTGCAG	250
388	CGACCCTTCT	CCTGGCATCG	TGGCATTTC	GAGATTGGAG	300
390	TAGATCCTGA	GAACATCACC	GAAATTTCA	TCGCAAACCA	350
392	GAAATCATCA	ACGAAGATGA	TGTTGAAGCT	TATGTGGGAC	400
394	GACAATTGTG	GATTCTGGAT	TAAAATTGT	GGCTCATAAA	450
396	AAAACAGCAA	CCTGCAGCAC	ATCAATTAA	CCCGAAACAA	500
398	TTGTCTAGGA	AACATTCCG	TCACCTTGAC	TTGTCTGAAC	550

VERIFICATION SUMMARY
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L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:36 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:40 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:44 M:220 C: Keyword misspelled or invalid format, [(viii) ATTORNEY/AGENT INFORMATION:]
L:49 M:220 C: Keyword misspelled or invalid format, [(ix) TELECOMMUNICATION INFORMATION:]
L:60 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=1